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RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/819,094

TIME: 10:12:44

Input Set : A:\UCSF-018-02US.txt

Output Set: N:\CRF3\10102001\I819094.raw

3 <110> APPLICANT: Weiner, Richard I.
4 Martial, Joseph A.
5 Struman, Ingrid
6 Taylor, Robert
7 Bentzien, Frauke
9 <120> TITLE OF INVENTION: Novel Antiangiogenic Peptide Agents and Their
10 Therapeutic and Diagnostic Use
12 <130> FILE REFERENCE: UCSF-018/02US
14 <140> CURRENT APPLICATION NUMBER: 09/819,094
15 <141> CURRENT FILING DATE: 2001-03-27
17 <150> PRIOR APPLICATION NUMBER: 09/076,675
18 <151> PRIOR FILING DATE: 1998-05-12
20 <150> PRIOR APPLICATION NUMBER: 60/046,394
21 <151> PRIOR FILING DATE: 1997-05-12
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27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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33 ttcgataaac ggtataccca tggccggggg ttcattacca aggccatcaa cagctgccac 180
34 acttcttccc ttgccacccc cgaagacaag gagcaagccc aacagatgaa tcaaaaagac 240
35 tttctgagcc tgatagtcag catattgcga tccctggaatg agcctctgta tcatctggtc 300
36 acggaagtac gtggtatgca agaagccccg gaggctatcc tatccaaagc tgtagagatt 360
37 gaggagcaaa ccaaacggct tctagagggc atggagctga tagtcagcca gggtcatcct 420
38 gaaaccaaag aaaatgagat ctaccctgtc tggctggggc ttccatccct gcagatggct 480
39 gatgaagaat ctgcctttc tgcctattat aacctgctcc actgcctacg caggcattca 540
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51 ttcgataaac ggtataccca tggccggggg ttcattacca aggccatcaa cagctccac 180
52 acttcttccc ttgccacccc cgaagacaag gagcaagccc aacagatgaa tcaaaaagac 240
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65 ttcgataaac ggtataccca tggccggggg ttcattacca aggccatcaa cagctccac 180
66 acttcttccc ttgccacccc cgaagacaag gagcaagccc aacagatgaa tcaaaaagac 240
67 tttctgagcc tgatagtcag catattgcga tcctggaatg agcctctgta tcatctggtc 300
68 acggaagtac gtggtatgca agaagccccg gaggctatcc tatccaaagc tgtagagatt 360
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80 ttcgataaac ggtataccca tggccggggg ttcattacca aggccatcaa cagctccac 180
81 acttcttccc ttgccacccc cgaagacaag gagcaagccc aacagatgaa tcaaaaagac 240
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86 gatgaagagt ctgccttttc tgcttattat aacctgctcc actgcctacg cagggattca 540
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98 aagctatttg ccatatgggt accggcccc aagtaatggt tccggtagtt gtcgacgggt 180
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100 aaagactcgg actatcagtc gtataacgct aggaccttac tcggagacat agtagaccag 300
101 tgccttcagt caccatacgt tcttcggggc ctccgatagg atagggttcg acatctctaa 360
102 ctctctggtt ggtttgccga agatctcccg tacctcgact atcagtcggg ccaagtagga 420
103 ctttggtttc ttttactcta gatgggacag accagccctg aaggtaggga cgtctaccga 480
104 ctacttctca gagcggaaag acgaataata ttggacgagg tgacggatgc gtcctaagt 540
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109 <211> LENGTH: 375
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115 ctggcgcggc agcaggacag ggtgatgtag gtattggaga ggagtcttta caagtcgctt 120
116 aagctatttg ccatatgggt accggcccc aagtaatggt tccggtagtt gtcgacgggt 180

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117 tgaagaaggg aacggtgggg gcttctgttc ctcggtcggg ttgtctactt agtttttctg 240
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130 aagctatttg ccatatgggt accggcccc aagtaatggt tccggtagtt gtcgacgggtg 180
131 tgaagaaggg aacggtgggg gcttctgttc ctcggtcggg ttgtctactt agtttttctg 240
132 aaagactcgg actatcagtc gtataacgct aggaccttac tcggagacat agtagaccag 300
133 tgccttcacg caccatacgt tcttcggggc ctccgatagg ataggtttcg acatctctaa 360
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145 aagctatttg ccatatgggt accggcccc aagtaatggt tccggtagtt gtcgacgggtg 180
146 tgaagaaggg aacggtgggg gcttctgttc ctcggtcggg ttgtctactt agtttttctg 240
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151 ctacttctca gagcggaag acgaataata ttggacgagg tgacggatgc gtccctaagt 540
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161 Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
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164 Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
165             20             25             30
167 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
168             35             40             45
170 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
171             50             55             60
173 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
174   65             70             75             80
176 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu

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179 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
180          100          105          110
182 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
183          115          120          125
185 Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu
186          130          135          140
188 Asn Glu Ile Tyr Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala
189 145          150          155          160
191 Asp Glu Glu Ser Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu
192          165          170          175
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195          180          185          190
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211          20          25          30
213 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
214          35          40          45
216 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
217          50          55          60
219 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
220 65          70          75          80
222 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
223          85          90          95
225 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
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228 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr
229          115          120
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233 <211> LENGTH: 140
234 <212> TYPE: PRT
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237 <400> SEQUENCE: 11
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241 Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
242          20          25          30
244 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
245          35          40          45
247 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
248          50          55          60

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250 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
251 65 70 75 80
253 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
254 85 90 95
256 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
257 100 105 110
259 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
260 115 120 125
262 Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro
263 130 135 140
266 <210> SEQ ID NO: 12
267 <211> LENGTH: 143
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275 Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
276 20 25 30
278 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
279 35 40 45
281 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
282 50 55 60
284 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
285 65 70 75 80
287 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
288 85 90 95
290 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
291 100 105 110
293 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
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308 cagaagtatt cgttcctgca tgactcccag acctccttct ctttctcaga ctctattccg 180
309 acaccctcca acatggagga aacgcaacag aaatccaatc tagagctgct ccgcatctcc 240
310 ctgctgctca tcgagtcgtg gctggagccc gtgcggttcc tcaggagtat gttcgccaac 300
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VERIFICATION SUMMARY DATE: 10/10/2001
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